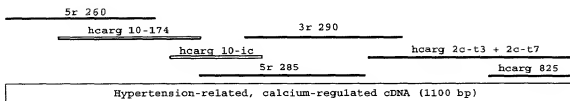


A



B

-131 SCACGAGCCACAGCCAGCTACCGCGCTAGGTTCTCTCCAGGTGCAAGAGGGG -80  
 GTAAAGGCTTGGTTGTATTGTAATGCAACTGTGGTTAGGACCTTCTCTCGGACTGGTCAAGAAACGGGAAGAAAGG -1  
 ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC -60  
 Met Ser Ala Leu Gly Ala Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly  
 CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG 120  
 Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu  
 AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT 180  
 Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His  
 GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC GCC AAC CTG TCA GAA GAG 240  
 Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu  
 CGT CTG GCC GTC CTG CTG GCG GGC ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC 300  
 Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro  
 CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG 360  
 Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln  
 GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT 420  
 Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser  
 GTA GCC CAA CAG CAG GGA TCC TCG CTG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480  
 Val Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp  
 GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CCG AGT GTT CTC ATG CAG CTG 540  
 Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu  
 AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600  
 Lys Leu Thr Asp Gly Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu  
 CGG TAC AGT GTA GCC TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660  
 Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg  
 AAA CTG CAG GAC TGA CTGAACCTGGTACTGTGGGTGCTGAAGCTGGTACCAAGAACACAGCCCCCACTGGGTGA 734  
 Lys Leu Gln Asp TER  
 TGAGCCCAACTCATTGAGGTCTCGCATGTGAGAACGTATTTAAGTGAAAAGACAGCGGACTTTTCAAGTCTTTGTTTT 813  
 ATGAGTCAACAGCTGGCGAGGTGGCACAGTTTATATCTCAGCCCTTGGAAGCTGAGGCTGGAGATGGGAAGTATA 892  
 AGCTGGGCTTGGCTTTCTAGTGAAGGCTCAGTGTGCAATTTAAAGAGGTAAAGCAATATTTAAAAAATTTTTAAAAA 969

FIGURE 1

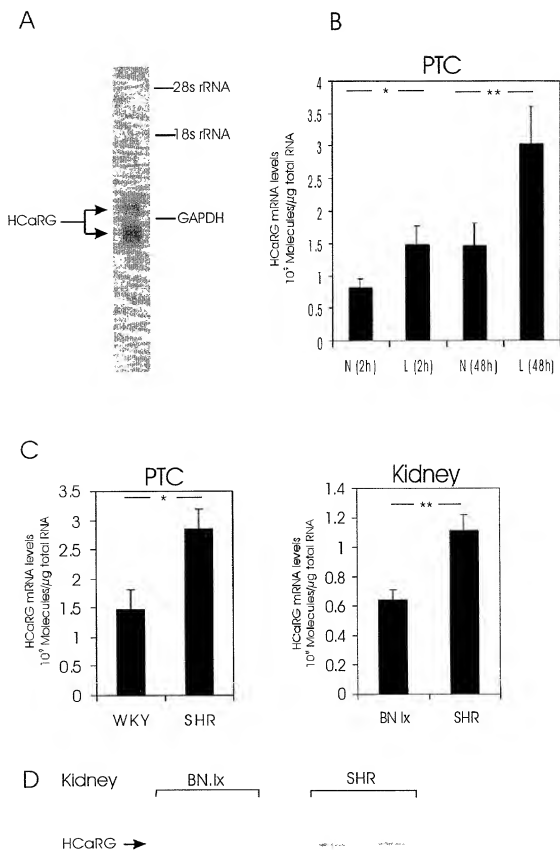


FIGURE 2

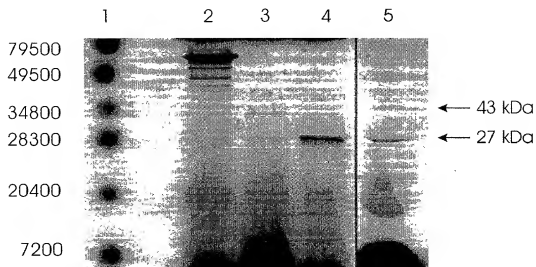


FIGURE 3

0304568.071501

rHcARG	MSAICAAAPY LHHHADSHSG RVSPFGSOPS	PEVTIAMAQLL KGLDRSTFRK	50
hHcARG	MSAVGAATPY LHHHGDSHSG RVSPFGAQLP	PEVAAMARLL GGLDRSTFRK	50
rHcARG	LLKIVVGATH GKDCREAVEQ LGASANTSEE	RLAVLLAGTH TMLQOALRLP	100
hHcARG	LLKFMVSSIQ GEDCREAVOR LGVSANTPEE	CLGALLAGMH TMLQOALRLP	100
rHcARG	PASLKPDATQ EELQELCLPQ DLTGDLASLA	FGSORPLIDS VAQOQGSLLP	150
hHcARG	PTSLKPDIER DQLQELCLPQ DLTGDLASVV	FGSORPLIDS VAQOQGAWLP	150
rHcARG	HVS YFRWRVD VATSTSAQSR SIQPSVLMQL KL	TDGSAHRE EVPIAKFOEL	200
hHcARG	HVADFRWRVD VATSTSALAR SIQPSVLMQL KL	TDGSAYRE EVPIAKFOEL	200
rHcARG	RYSVALVLKE MADLEKKOER KLQD		224
hHcARG	RYSVALVLKE MADLEKKOER KLQD		224

FIGURE 4

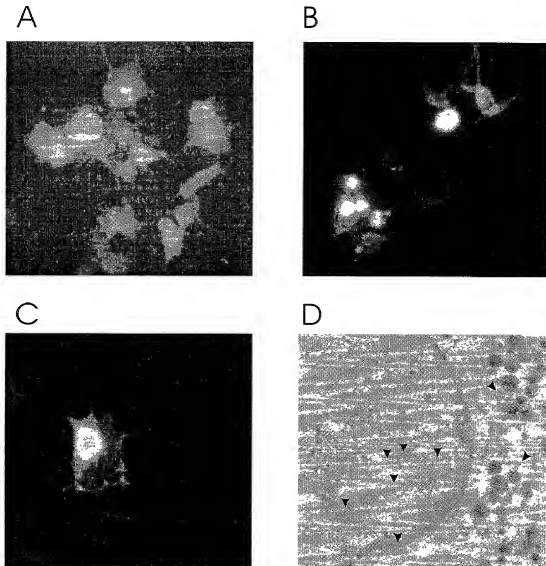
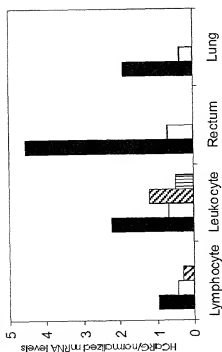
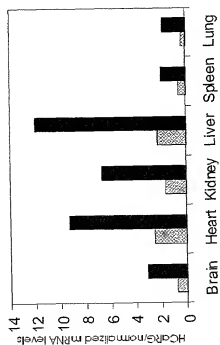


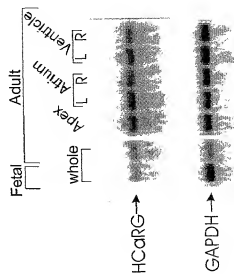
FIGURE 5

# FIGURE 6: HCaRG Normal/Cancerous

## A Fetal/Adult



## B HEART



## D Tumor/Normal

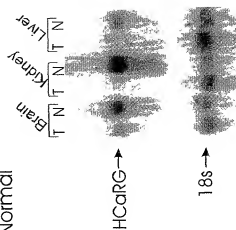


FIGURE 6

Antisense  
 09004568-071611  
 sense

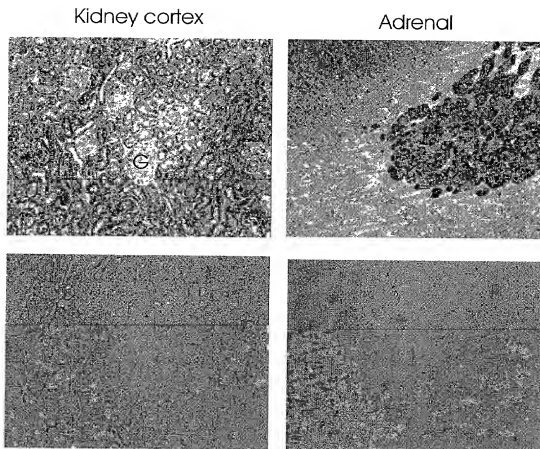
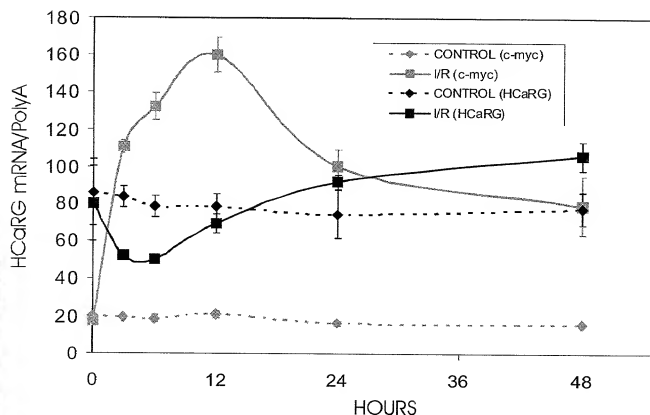
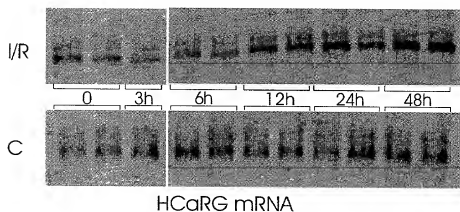


FIGURE 7

# A Medulla



# B Cortex



# C Cortex

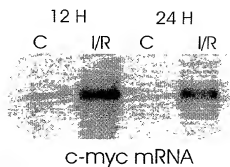
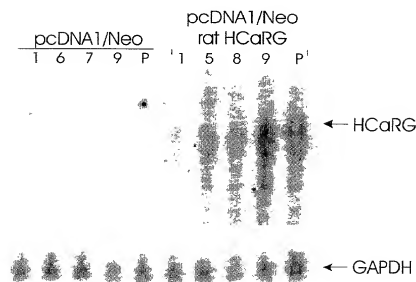


FIGURE 8



A



B

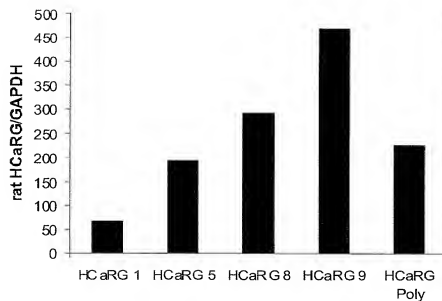
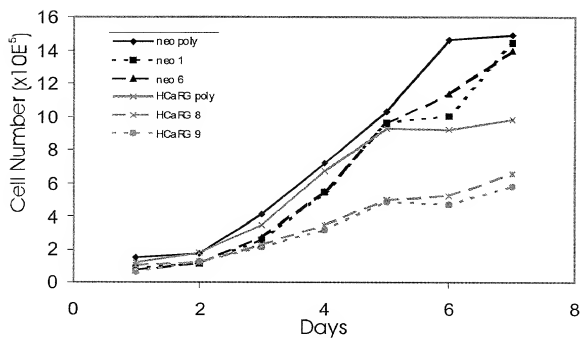


FIGURE 9

A



B

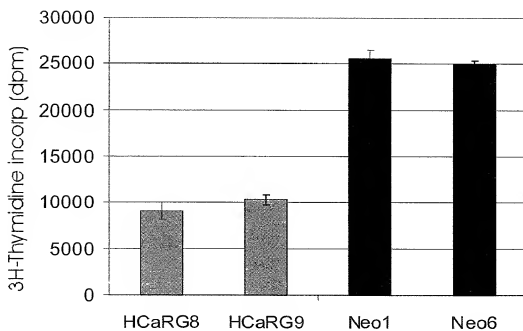


FIGURE 10

109120' 89540660

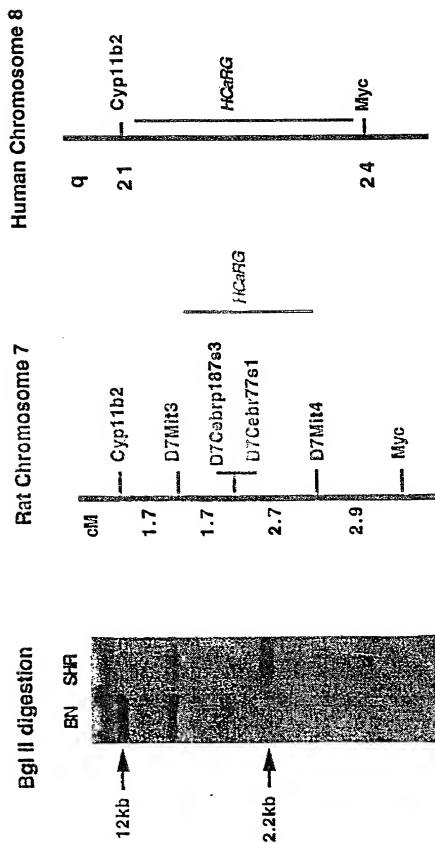


FIGURE 11